Multiscale Functional-Structural Plant Modelling at the Example of Apple Trees

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Introduction

This is a description of an ongoing project which aims at understanding the development and functioning of apple trees by modelling them at several spatial and temporal scales. Dependence of growth and carbon allocation upon genotype, environmental variables, fruit load and experimental manipulation of carbon transport is investigated and simulated. For the required functional-structural models, new tools are developed, especially for handling multiple-scale representations of the same organism in a user-friendly way. This joint project (French-German) brings together expertise in botany, eco-physiology, horticultural tree modelling, mathematics and computer science. The following gives short outlines of the research, planned and partially completed, in the four work packages which correspond to the principal partners (University of Göttingen, Göttingen Agrocampus Ouest, Angers, INRA, Montpellier, and CentraleSupélec, Paris).

Work Packages Outline

WORK PACKAGE 1

A. *Provide tools for working with multiple scales*
- development of software tools for simultaneous handling of fruit trees at several structural scales within FSPMs
- methods for upscaling (aggregating microscale information to a macroscale) and downscaling (the reverse information flow) for plant structures and for processes affecting plants
- meta-modelling - the aggregated description of the output of a fine-scale model by a simpler model at a coarser scale

B. *Case studies*
- tools evaluated at an integrated multiscale model of apple branch physiology and organ development
- compare several, alternative components for light interception, water and carbon transport at different scales
- evaluate the benefits and drawbacks of modelling at finer scales

C. *Platform interfacing*
- interfaces between GroIMP and OpenAlea and between GroIMP and PYGMALION are currently being developed and tested

WORK PACKAGE 2

A. *Branch model – concept*
- aims at the conceptualization and subsequent implementation of a functional-structural plant model of the bearing branch of apple, with a strong emphasis on combined carbon and water flows between sources (leaves) and sinks (developing fruits) within the same branch (cf. [1]).

B. *Branch model – development*
- to elucidate and quantify the influence of the topological and geometrical distribution of source and sink organs within a branch, by achieving a better description of combined sugar and water transport

Fig. 1 Experiments used to follow C transport in the branch of apple tree: $^{13}CO_2$ labelling with LI-6400XT portable photosynthesis system.

WORK PACKAGE 3

A. *Tree model – environmental influence*
- aims at modelling the genotypic variability of the apple tree architecture development taking into account environmental effects
- model the phytomer appearance rate of the shoot and the probability of appearance of sylleptic shoots along the trunk of one-year-old apple scions, and to estimate a set of genotypic model parameters

B. *Tree model – genetic influence*
- study the genetic determinisms of those parameters based on previously available genotyping data of the progeny including 2K single-nucleotide polymorphisms (SNPs)
- use of a genome wide association method used to estimate markers effects. The accuracy of this model was evaluated by a k fold cross-validation
- prediction of the parameters based on markers effects is currently implemented in the functional-structural apple tree model, MAppleT [2].

WORK PACKAGE 4

A. *Parameter estimation by Bayesian methods*
- translate the models in the framework of hidden Markov models
- state of the art methods for parameter inference are currently being tested in the context of FSPM

B. *Sensitivity analysis*
- use of 'Factor Fixing Setting' for non-influential parameters
- development of variance decomposition methods for sensitivity analysis, adapted to correlated inputs

Bayesian estimation and sensitivity analysis are implemented in the modelling platform PYGMALION

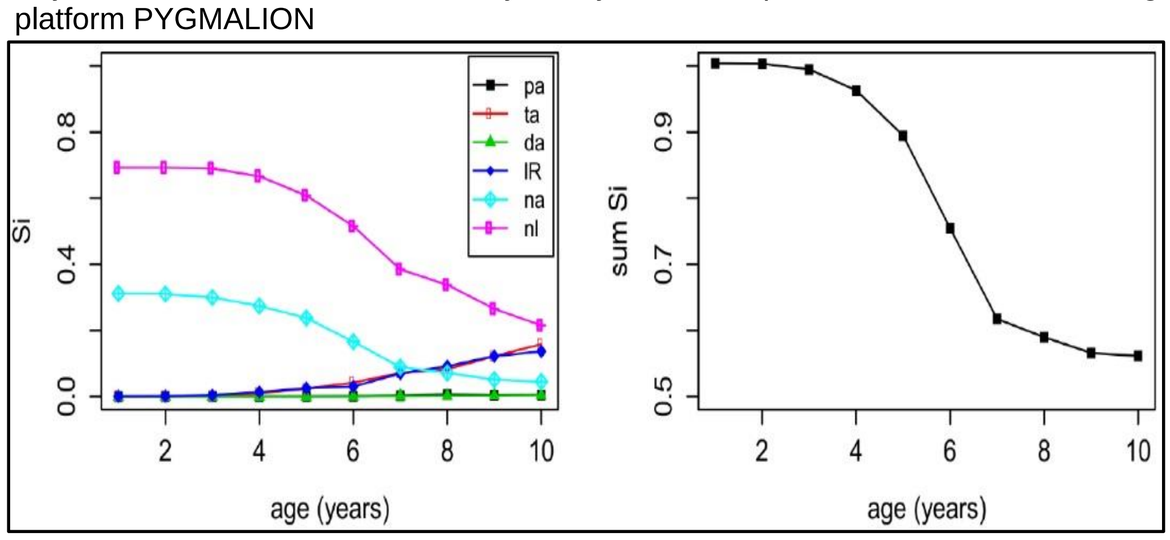

Fig. 2 Sensitivity analysis run on PYGMALION based on a GroIMP model. The colors correspond to different parameters of the model.

GROIMP OPENALEA INTERFACE

- development of an interface for data exchange using a file format compliant with the generic XML syntax [3]
- design of a web-based communication workflow adopting the standardized HTTP protocol
- the design includes the creation of two interfacing packages on top of both GroIMP and OpenAlea [3,4,5].
- it consists of a communication layer and an information transformation layer
- the GroIMP-OpenAlea interface could serve as a prototype for a general framework for communication and data exchange among diverse modelling platforms, e.g. cross-platform modelling with different FSPMs

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